

**Amendments to the Claims:**

Please amend Claims 1, 89 and 90.

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

1. (Currently Amended) A method of inferring, with a predetermined level of confidence, proportional ancestry of at least two ancestral groups of a test individual by identification of a population structure comprising:
  - a) determining single nucleotide polymorphisms (SNPs) for a first population and identifying a first population of SNPs having a frequency differential ( $\delta$ )  $> 0.4$  between one or more pairs of population groups wherein the first population of SNPs are identified from a database *in silico*;
  - b) contacting a parental sample nucleic acid with one or more hybridizing nucleic acids corresponding the first population of SNPs, wherein the one or more hybridizing nucleic acids selectively hybridize to the nucleic acid in the parental sample;
  - c) selecting SNPs hybridizing in step (b) to generate a second population of SNPs which have a minor allele frequency  $> 1\%$  and a  $\delta > 0.4$  for at least one pair of the at least two population groups, wherein
    - (i) at least one of the second population of SNPs is a SNP which may be correlated with but not linked to a gene-linked trait,
    - (ii) the second population of SNPs comprise autosomal markers, and
    - (iii) at least one SNP of the second population of SNPs is not located within a region of a gene encoding a protein;
  - d) contacting a sample comprising nucleic acid molecules of a test individual with at least 20 second population of SNPs, wherein the second population of SNPs are indicative of a population structure, and wherein the population structure is

- correlated with a trait of the test individual, wherein the trait comprises biogeographical ancestry (BGA);
- e) determining the nucleotide occurrences of the second population of SNPs in the sample from the test individual;
  - f) identifying the population structure indicated by the nucleotide occurrences determined for the test individual, wherein identifying the population structure infers the proportional ancestry of at least two ancestral groups of the test individual, comprising:
    - (i) performing six two-way comparisons, three three-way comparisons, or one four-way comparison among ancestral groups;
    - (ii) determining a likelihood of all possible proportional affiliations among four ancestral groups having the greatest likelihood values, ~~whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the test individual is identified~~ correlating population structure with nucleotide occurrences; and
    - (ii) identifying a single proportional combination of maximum likelihood; and
  - g) providing information resulting from steps (a) through (f) to a user.

2-83. (Canceled)

84. (Previously presented) The method of claim 1, wherein the identifying step (a) comprises demonstrating a  $\delta > 0.4$  between any two of four intercontinental or intracontinental population groups or determining an  $F_{st} > 0.4$  at an average spacing of about 2-3 cM between any two of four intercontinental or intracontinental population groups.
85. (Previously presented) The method of claim 1, wherein the one or more pairs is from at least two intercontinental or intracontinental population groups.

86. (Previously presented) The method of claim 84, wherein the parental sample is from a human individual determined to be a Sub-Saharan African, an IndoEuropean, an East Asian, a Native American, a Northern European, a Continental European, an Iberian, a Northeastern European, a Middle Eastern European, a South Asian European, or a Southeastern European.
87. (Previously presented) The method of claim 1, wherein the sample of step (d) is contacted with at least 200 second population SNPs.
88. (Previously presented) The method of claim 1, wherein the sample of step (d) is contacted with at least 100 second population SNPs.
89. (Currently Amended) The method of claim 1, wherein the sample of step (d) is contacted with a second population of SNPs selected from the group consisting of SEQ ID NOs: 1 to 331.
90. (Currently Amended) The method of claim 1, wherein the second population SNPs ~~comprise~~ is selected from the group consisting of SEQ ID NOs: 1 to 331.
91. (Previously presented) The method of claim 1, wherein proportional ancestry is determined by employing an algorithm which maximizes a cumulative  $\delta$  value between, and minimizes a difference in cumulative  $\delta$  value within, each of the one or more pairs of the population groups.
92. (Previously presented) The method of claim 91, wherein the algorithm inverts population specific allele frequencies, thereby obtaining a likelihood estimate, or a likelihood based estimate, of proportional ancestry corresponding to a multilocus genotype.

93. (Previously presented) The method of claim 92, wherein the likelihood estimate is measured for at least three of the intercontinental or intracontinental population groups simultaneously.
94. (Previously presented) The method of claim 93, wherein the estimate is repeated for all possible intercontinental or intracontinental population groups.
95. (Previously presented) The method of claim 85, wherein the intercontinental or intracontinental population groups are selected from the group consisting of Sub-Saharan African, IndoEuropean, East Asian, Native American, Northern European, Continental European, Iberian, Northeastern European, Middle Eastern European, South Asian European, and Southeastern European.
96. (Previously presented) The method of claim 1, wherein the BGA comprises a proportion of Sub-Saharan African, IndoEuropean, East Asian, Native American, Northern European, Continental European, Iberian, Northeastern European, Middle Eastern European, South Asian European, or Southeastern European ancestral groups, or a combination thereof.
97. (Previously presented) The method of claim 1, wherein second population SNPs comprise SEQ ID NOs: 1 to 71.
98. (Previously presented) The method of claim 96, further comprising performing a likelihood determination for affiliation with each of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, and an East Asian ancestral group;  
selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the test individual is identified; and

identifying a single proportional combination of maximum likelihood.

99. (Previously presented) The method of claim 96, further comprising performing six two-way comparisons comprising likelihood determinations for affiliation between each group with each other group;

selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the test individual is identified; and

identifying a single proportional combination of maximum likelihood.

100. (Previously presented) The method of claim 96, further comprising

performing three three-way comparisons among the groups;

determining a likelihood of all possible proportional affiliations among three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the test individual is identified; and

identifying a single proportional combination of maximum likelihood.

101. (Cancelled)

102. (Previously presented) The method of claim 1, further comprising generating a graphical representation of the comparison of the three ancestral groups, the graphical

representation comprising a triangle with each ancestral group independently represented by a vertex of the triangle, wherein the maximum likelihood value of proportional affiliation for a test individual comprises a point within the triangle.

103. (Previously presented) The method of claim 102, wherein the graphical representation further comprises a confidence contour indicating a level of confidence associated with estimating the proportional ancestry.
104. (Previously presented) The method of claim 96, further comprising identifying an ethnicity of the test individual, which comprises identifying a subpopulation structure of the population structure indicated by the nucleotide occurrences of the SNPs detected in the test individual, wherein the SNPs are further indicative of a sub-population structure, and wherein the sub-population structure infers ethnicity of the test individual.
105. (Previously presented) The method of claim 104, wherein the ancestral group is IndoEuropean, and wherein the ethnicity comprises Northern European or Mediterranean.
106. (Previously presented) The method of claim 96, further comprising generating an ancestral map of the world, wherein locations of populations having a proportional ancestry corresponding to the proportional ancestry of the individual are indicated on the ancestral map.
107. (Previously presented) The method of claim 96, wherein the step (f) identifying a population structure indicated by the nucleotide occurrences determined for the test individual comprises comparing the nucleotide occurrences of the SNPs detected in the test individual with known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA.

108. (Previously presented) The method of claim 107, wherein the known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA are contained in a database.
109. (Previously presented) The method of claim 108, wherein the comparing is performed using a computer.
110. (Previously presented) The method of claim 107, wherein each of the known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA further comprises at least one photograph of a person from whom the known proportional ancestry was determined.
111. (Previously presented) The method of claim 110, wherein the at least one photograph comprises a digital photograph.
112. (Previously presented) The method of claim 111, wherein digital information comprising the digital photograph is contained in a database.
113. (Previously presented) The method of claim 112, wherein the digital information in the database is associated with the known proportional ancestry corresponding to nucleotide occurrences of SNPs indicative of BGA of the person in the photograph.
114. (Previously presented) The method of claim 108, further comprising identifying at least one photograph of a person having a proportional ancestry corresponding to the proportional ancestry of the test individual.
115. (Previously presented) The method of claim 114, wherein identifying the photograph comprises scanning a database comprising a plurality of files, each file comprising digital

information corresponding to a digital photograph of a person having a known proportional ancestry, and identifying at least one photograph of a person having nucleotide occurrences of SNPs indicative of BGA that correspond to the nucleotide occurrences of SNPs indicative of BGA of the test individual.